

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=4; day=25; hr=14; min=3; sec=3; ms=423;]

=====

Application No: 10539962 Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-14 16:27:59.858
Finished: 2008-04-14 16:28:01.311
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 453 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 37
Actual SeqID Count: 37

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)

Input Set:

Output Set:

Started: 2008-04-14 16:27:59.858
Finished: 2008-04-14 16:28:01.311
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 453 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 37
Actual SeqID Count: 37

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> FAGAN, RICHARD JOSEPH
PHELPS, CHRISTOPHER BENJAMIN
RODRIGUES, TANIA MARIA
POWER, CHRISTINE
DE TIANI, MARIASTELLA

<120> SPLICE VARIANT OF HUMAN PLACENTAL GROWTH HORMONE

<130> C&R-106

<140> 10539962
<141> 2008-04-14

<150> PCT/GB03/05594
<151> 2003-12-19

<150> GB 0229850.3
<151> 2002-12-20

<160> 37

<170> SeqWin99, version 1.02

<210> 1
<211> 180
<212> DNA
<213> Homo sapiens

<400> 1
gctcccgac gtccctgctc ctggcttttg gcctgctctg cctgtcctgg cttcaagagg 60
gcagtgcctt cccaaaccatt cccttatcca ggcttttga caacgctatg ctccgcgcc 120
gtcgcctgta ccagctggca tatgacacacct atcaggagtt tgtaagctct tgggtaatgg 180

<210> 2
<211> 60
<212> PRT
<213> Homo sapiens

<400> 2
Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Ser Trp
1 5 10 15

Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
20 25 30

Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp
35 40 45

Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu
50 55 60

<210> 3
<211> 47
<212> DNA

<213> Homo sapiens

<400> 3

agtctattcc aacacaccttcc aacagggtga aaacgcagca gaaatct 47

<210> 4

<211> 15

<212> PRT

<213> Homo sapiens

<400> 4

Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser

1 5 10 15

<210> 5

<211> 227

<212> DNA

<213> Homo sapiens

<400> 5

gctcccgac gtccctgctc ctggcttttg gcctgctctg cctgtcctgg cttcaagagg 60

gcagtcgcctt cccaaccatt cccttatcca ggcttttga caacgctatg ctccgcgc 120

gtcgctgtatccagctggca tatgacacct atcaggagtt tgtaagctct tggtaatgg 180

agtctattcc aacacaccttcc aacagggtga aaacgcagca gaaatct 227

<210> 6

<211> 75

<212> PRT

<213> Homo sapiens

<400> 6

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Ser Trp

1 5 10 15

Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe

20 25 30

Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp

35 40 45

Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu Ser Ile Pro Thr

50 55 60

Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser

65 70 75

<210> 7

<211> 600

<212> DNA

<213> Homo sapiens

<400> 7

atggctgcac gctcccgac gtccctgctc ctggcttttg gcctgctctg cctgtcctgg 60

cttcaagagg gcagtcgcctt cccaaccatt cccttatcca ggcttttga caacgctatg 120

ctccgcgc 180

gtcgctgtatccagctggca tatgacacct atcaggagtt tgtaagctct tggtaatgg 240

cttagagctgc tccgcatctc cctgctgctc atccagtcat ggctggagcc cgtgcagctc 300

ctcaggagcg tcttcgccaa cagcctggtg tatggcgccct cggtacagcaa cgtctatcg 360
cacctgaagg accttagagga aggcattccaa acgtgtatgt ggaggctgga agatggcagc 420
ccccggactg ggcagatctt caatcagtcc tacagcaagt ttgacacaaa atcgacaaac 480
gatgacgcac tgctcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag 540
gtcgagacat tcctgcgcac cgtgcagtgc cgctctgtgg agggcagctg tggcttctag 600

<210> 8
<211> 199
<212> PRT
<213> Homo sapiens

<400> 8
Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln
35 40 45

Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu
50 55 60

Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn
65 70 75 80

Leu Glu Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu
85 90 95

Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly
100 105 110

Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly
115 120 125

Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly
130 135 140

Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn
145 150 155 160

Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys
165 170 175

Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser
180 185 190

Val Glu Gly Ser Cys Gly Phe
195

<210> 9
<211> 522
<212> DNA
<213> Homo sapiens

<400> 9

ttcccaacca ttcccttatac caggctttt gacaacgcta tgctccgcgc ccgtcgccctg 60
taccagctgg catatgacac ctatcaggag tttgtaagct cttggtaat ggagtctatt 120
ccaacacacctt ccaacagggt gaaaacgcac cagaaatcta acctagagct gctccgcac 180
tccctgtgc tcatacgttc atggctggag cccgtgcacg tcctcaggag cgtcttcgccc 240
aacagcctgg tgtatggcgc ctcggacagc aacgtctatc gccacctgaa ggacctagag 300
gaaggcatcc aaacgctgat gtggaggctg gaagatggca gccccggac tgggcagatc 360
ttcaatcagt cctacagcaa gtttgacaca aaatcgacaa acgtgacgc actgctcaag 420
aactacgggc tgctctactg cttcaggaag gacatggaca aggtcgagac attcctgcgc 480
atcgtgcagt gccgctctgt ggagggcagc tgtggcttct ag 522

<210> 10
<211> 173
<212> PRT
<213> Homo sapiens

<400> 10
Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
1 5 10 15

Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val
20 25 30

Ser Ser Trp Val Met Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys
35 40 45

Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu
50 55 60

Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala
65 70 75 80

Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu
85 90 95

Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp
100 105 110

Gly Ser Pro Arg Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe
115 120 125

Asp Thr Lys Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu
130 135 140

Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg
145 150 155 160

Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
165 170

<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GCP Forward

<400> 11
ggggacaagt ttgtacaaaa aaggcaggctt cgccacc 37

<210> 12
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GCP Reverse

<400> 12
ggggaccact ttgtacaaga aagctgggtt tcaatggtga tggtgatgg 51

<210> 13
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105-exon2F

<400> 13
gcaggcttcg ccaccatggc tgcaggctcc cggacgtccc tgctcctg 48

<210> 14
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105-exon2R

<400> 14
ggaaggtgtt ggaatagact ccattaccca agagctta 38

<210> 15
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105- exon3F

<400> 15
agctcttggg taatggagtc tattccaaca ccttcc 36

<210> 16
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105- exon3R

<400> 16
ggagcagctc taggttagat ttctgctgcg ttttca 36

<210> 17
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105- exon4F

<400> 17
aacgcagcag aaatctaacc tagagctgct ccgcatac 37

<210> 18
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105- exon4R

<400> 18
tgccatttc cagcctccac atcagcggtt ggatgc 36

<210> 19
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105- exon5F

<400> 19
ccaaacgctg atgtggaggc tggaaagatgg cagccc 36

<210> 20
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105- exon5R

<400> 20
gtgatggta tgggtggaaagc cacagctgcc ctcca 35

<210> 21
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105-5' end-R

<400> 21
ggtagattt ctgctgcgtt ttccccctgt tg 32

<210> 22

<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105-center-F

<400> 22
caacagggtg aaaacgcagc agaaaatctaa cc 32

<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105-center-R

<400> 23
ggctgccatc ttccagcctc ca 22

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer INSP105-3' end-F

<400> 24
gcatccaaac gctgatgtgg ag 22

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer pEAK12-F

<400> 25
gccagcttgg cacttgatgt 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer pEAK12-R

<400> 26
gatggaggtg gacgtgtcag 20

<210> 27
<211> 18
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer M13F

<400> 27

caggaaacag ctagacc

18

<210> 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer M13R

<400> 28

tgtaaaacga cggccagt

18

<210> 29

<211> 129

<212> DNA

<213> Homo sapiens

<400> 29

tccctgctgc tcatccagtc atggctggag cccgtgcagc tcctcaggag cgtttcgcc
aacagcctgg tgtatggcgc ctcggacagc aacgtctatac gccacctgaa ggacctagag
gaaggcatc

60

120

129

<210> 30

<211> 217

<212> PRT

<213> Homo sapiens

<400> 30

Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu

1 5 10

15

Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu

20 25

30

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln

35 40 45

Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Leu Lys

50 55 60

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe

65 70 75 80

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys
85 90 95

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110

Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val
115 120 125

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu
130 135 140

Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160

Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser
165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe
210 215

<210> 31

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> Exon

<222> (1)..(597)

<400> 31

atg gct gca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc
Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

48

tgc ctg tcc tgg ctt caa gag ggc agt gcc ttc cca acc att ccc tta
Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30

96

tcc agg ctt ttt gac aac gct atg ctc cgc gcc cgt cgc ctg tac cag
Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln

144

35	40	45	
ctg gca tat gac acc tat cag gag ttt gta agc tct tgg gta atg gag Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu			192
50	55	60	
tct att cca aca cct tcc aac agg gtg aaa acg cag cag aaa tct aac Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn			240
65	70	75	80
cta gag ctg ctc cgc atc tcc ctg ctc atc cag tca tgg ctg gag Leu Glu Leu Leu Arg Ile Ser Leu Leu Ile Gln Ser Trp Leu Glu			288
85	90	95	
ccc gtg cag ctc ctc agg agc gtc ttc gcc aac agc ctg gtg tat ggc Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly			336
100	105	110	
gcc tcg gac aac gtc tat cgc cac ctg aag gac cta gag gaa ggc Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly			384
115	120	125	
atc caa acg ctg atg tgg agg ctg gaa gat ggc agc ccc cgg act ggg Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly			432
130	135	140	
cag atc ttc aat cag tcc tac agc aag ttt gac aca aaa tcg cac aac Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn			480
145	150	155	160
gat gac gca ctg ctc aag aac tac ggg ctg ctc tac tgc ttc agg aag Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys			528
165	170	175	
gac atg gac aag gtc gag aca ttc ctg cgc atc gtg cag tgc cgc tct Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser			576
180	185	190	
gtg gag ggc agc tgt ggc ttc Val Glu Gly Ser Cys Gly Phe			597
195			
<210> 32			
<211> 597			
<212> DNA			
<213> Homo sapiens			
<400> 32			
ctggctgcag gctccggac gtcctgtctc ctggcttttg gcctgtctg cctgtctgg			60
cttcaagagg gcagtgcctt cccaaccatt cccttatcca ggcttttga caacgctatg			120
ctccgcgcc gtcgctgtt ccagctggca tatgacacct atcaggagtt tgtaagctt			180
tgggtaatgg agtctattcc aacaccttcc aacagggtga aaacgcagca gaaatctcac			240

ctagagctgc tccgcatctc cctgctgctc atcgagtgt ggctggagcc cgtgcagttc 300
ctcaggagtg tcttcgccaa cagcctggtg tacggcgct ctgacagcaa cgtctatgac 360
ctcctaaagg acctagagga aggcataccaa acgctgatgt ggaggctgga agatggcagc 420
ccccggactg ggcagatctt caagcagacc tacagcaagt ttgacacaaa ctcgcacaac 480
catgacgcac tgctcaagaa ctacggctg ctccactgct tcaggaagga catggacaag 540
gtcgagacat tcctgcgcat cgtgcagtgc cgctctgtgg agggcagctg tggcttc 597

<210> 33
<211> 589
<212> DNA
<213> Homo sapiens

<400> 33
atggctccgg acgtccctgc tctggcttt tggcctgctc tgcctgcctt ggcttcaaga 60
gggcagtgcc ttcccaacca ttcccttatac caggctttt gacaacgcta tgctccgcgc 120
ccatcgctcg caccagctgg ctttgacac ctaccaggag ttgttaagct ctgggtaat 180
ggagtctatt ccaacacctt ccaacagggt gaaaccgcag cagaaatcta acctagagct 240
gctccgcata tccctgctgc tcatccagtc atggctggag cccgtgcagc tcctcaggag 300
cgtcttcgccc aacaggctgg tgtatggcgc ctggacagc aacgtctatac gccacctgaa 360
ggaccttagag gaaggcatcc aaacgctgat gtggaggctg gaagatggca gccacctgac 420
tggcagacc ctcaaggaga cctacagcaa gttgacacaca aactcgacaca accatgacgc 480
actgctcaag aactacgggc tgctccactg cttcaggaag gacatggaca aggtcgagac 540
attcctgcgc atcgtgcagt gcccgtctgt ggaggcga